<151> 2000-02-22

<150> 60/241,916 <151> 2000-10-18

<213> Homo sapiens

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Cys Lys Xaa Xaa Gln Cys Ser Phe Xaa Xaa Ala Arg Xaa Ile Phe Lys 20 25 30

Asp Ala Xaa Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp 35 40 45

Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
50 55 60

Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn 65 70 75 80

Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly 85 90 95

Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
100 105 110

Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr 115 120 125

Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg 130 135 140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro 145 150 155 160

Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln
165 170 175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala 180 185 190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu 195 200 205

Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg 210 215 220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn 225 230 235 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp 245 250 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr 260 265 . 270

Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu 275 280 285

Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg

290 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser 305 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser 330 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile 370 Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro 405 <210> 2 <211> 1338 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (115)..(1332) <400> 2 atgqtcaqcc aggccctccg cctcctgtgc ctgctcctgg ggctgcaggg ctgcctggct 60 qccqtcttcq tcacccaqqa qqaaqcccat ggcgtcctgc atcgccggcg ccgg gcc 117 Ala aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc 165 Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac 213 Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp 20 gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag 261 Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln 40 35 309 tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu 60 50 55

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											aac Asn					405
											aag Lys		Ser			453
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											gtg Val					693
		_	_		_						atc Ile 205	_	_			741
gaa Glu 210	cac His	gat Asp	ctg Leu	tcc Ser	gag Glu 215	cat His	gac Asp	gly ggg	gac Asp	gaa Glu 220	cag Gln	tcc Ser	cgc Arg	cgg Arg	gtg Val 225	789
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Val	Val	Pro 260	Leu	Cys	Leu	Pro	Glu 265	Arg	Thr	Phe	agc Ser	Glu 270	Arg	Thr	Leu	933
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	acc Thr															1077
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	agc Ser															1173
	acc Thr 355							_	_			_		_	_	1221
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Cys	Lys	Glu	Glu 20	Gln	Cys	Ser	Phe	Glu 25	Glu	Ala	Arg	Glu	Ile 30	Phe	Lys	•
Asp	Ala	Glu	Ara	Thr	Lys	Leu	Phe	Trp	Ile	Ser	Tyr	Ser	Asp	Gly	Asp	

Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp 35 40 45

Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
50 60

Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn 65 70 75 80

Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly 85 90 95

- Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
  100 105 110
- Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr 115 120 125
- Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg 130 135 140
- Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro 145 150 155 160
- Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Val Asn Gly Ala Gln
  165 170 175
- Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala 180 185 190
- His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu 195 200 205
- Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg 210 215 220
- Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn 225 230 235 240
- His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp 245 250 255
- His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr 260 265 270
- Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu 275 280 285
- Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg 290 295 300
- Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser 305 310 315 320
- Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser 325 330 335
- Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr 340 345 350
- Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys 355 360 365
- Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile  $370 \hspace{1cm} 375 \hspace{1cm} 380$
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gegeegggee aatgeettte tggaagaget eegeeetgge teeetggaac gegaatgeaa 180
agaggaacag tgcagctttg aggaaqcccq qqagattttc aaaqacqctq aqcqqaccaa 240
actgttttgg attagctata gcgatggcga tcagtgcgcc tccagccctt gccaqaacgg 300
gggctcctqc aaagaccagc tgcagagcta tatctgcttc tgcctgcctg cctttgaggg 360
gcgcaattgc gaaacccata aggatgacca gctgatttgc gtcaacgaaa acqqqqctq 420
cgagcagtac tgcagcgatc acacgggcac gaagcggagc tgccgctgcc acgaaggcta 480
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cggcgggacc ctcatcaata ccatttgggt cgtgtccgcc gctcactgct tcgataagat 720
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ggacgaacag tcccgccggg tggctcaggt catcattccc tccacctatg tgcctggcac 840
gaccaatcac gatategete tgeteegeet ceaceageee gtegtgetea eegateaegt 900
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tagcctcgtg tccggctggg gccagctgct cgaccggggc gctaccgctc tcgagctgat 1020
ggtgctcaac gtccccggc tgatgaccca ggactgcctg cagcagtccc gcaaagtggg 1080
ggactccccc aatatcacgg agtatatgtt ttgcgctggc tatagcgatg gctccaagga 1140
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His His His His His
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Met Lys His His His His His
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Asp Tyr Lys Asp Asp Asp Lys
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